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(54) **Rhesus ob protein and DNA**

(57) The invention includes proteins, pharmaceutical formulations, and methods useful for expressing pro-

teins that regulate the body's volume of adipose tissue.  
In particular, the *Rhesus ob* gene and gene product are  
disclosed.

EP 0 744 408 A2

## Description

The invention belongs to the general field of molecular biology as applied to biopharmaceutical research and development. The invention includes nucleic acid compounds, vectors and methods useful for expressing proteins that help regulate the body's volume of adipose tissue.

Obesity, especially upper body obesity, is a common and very serious public health problem in the United States and throughout the world. According to recent statistics, more than 25% of the U.S. population and 27% of the Canadian population are over weight. Kuczmarski, *Amer. J. of Clin. Nut.* 55: 495S - 502S (1992); Reeder *et al.*, *Can. Med. Ass. J.*, 23: 226-233 (1992). Upper body obesity carries the highest risk factor known for Type II Diabetes and is a significant risk factor for cardiovascular disease and cancer as well. Recent cost estimates for medical complications associated with obesity are \$150 billion world wide. The problem has now become so serious that the Surgeon General has begun a national initiative to combat obesity in America.

Hypertension, dyslipidemia, and insulin resistance are the primary pathologies associated with obesity. Many studies have demonstrated that weight reduction through diet and exercise dramatically improves these serious medical conditions. Unfortunately, obese individuals generally fail to significantly reduce their body mass through diet and exercise and have a near 95% failure rate. This failure may be due to genetically inherited factors that contribute to increased appetite, preference for high calorie foods, reduced physical activity, reduced lipolytic metabolism, and increased lipogenic metabolism. This indicates that people inheriting these genetic traits are prone to becoming obese regardless of their efforts to combat the condition. Therefore, new pharmacological agents that can reverse obesity in spite of genetic predisposition are needed.

The *ob/ob* mouse model of obesity and diabetes is known to carry an autosomal recessive trait linked to a mutation in the sixth chromosome. Recently, Zhang and coworkers published the positional cloning of a mouse gene linked to this condition. Zhang *et al.* *Nature* 372: 425-32 (1994). This report discloses a mouse cDNA sequence encoding a 167 amino acid protein that is expressed exclusively in adipose tissue and compares this mouse *ob* gene product to a human homolog. The report also discloses a point mutation resulting in the conversion of an Arg codon to a stop codon at position 105. This mutant gene is postulated to express a truncated protein that lacks the biological function of the complete intact protein.

Physiologists have long postulated that excess fat cells laid down through overeating signals the brain that the body is obese which, in turn, causes the body to eat less and burn more fuel. G. R. Hervey, *Nature* 227: 629-631 (1969). Parabolic experiments support a "feedback" model and suggest that a circulating peptide hormone may regulate the size of the body's fat depot. The newly disclosed *ob* gene product mentioned above is now believed to be such a hormone.

The present invention is based on the discovery of an obesity gene cloned from *Rhesus* monkey adipose tissue. Therefore, this invention is useful for producing what is currently believed to be a biologically active anti-obesity protein useful for treating obesity and reducing the risk for Type II diabetes, cardiovascular diseases, and cancer in mammals. It is also contemplated that conservative amino acid substitutions may be made to the protein in quiet regions without significantly altering biological activity. Consequently, analogous alterations at the DNA level to effect such substitutions are also contemplated.

The invention is also useful in a *Rhesus* immunogenicity model. In this mode, the invention can be used to predict the immunogenic capacity of analogs of the human *ob* gene product. For example, if one wished to determine whether a specific substitution in the human *ob* gene product would produce an antibody response in humans, the corresponding substitution could be made in the *Rhesus* *ob* protein. The *Rhesus* analog is then injected into a *Rhesus* monkey and its immunological response monitored. If the substitution failed to produce an immunological response, one would then accurately predict that the corresponding substitution in the human *ob* protein also would not raise an immunological response in a human.

The present invention is directed to a biologically active protein of SEQ ID NO: 2, and DNA encoding same as well as production methods. The invention further provides a method of treating obesity, which comprises administering to a warm-blooded animal in need thereof a protein of SEQ ID NO: 2. The invention further provides formulations, which comprise a protein of SEQ ID NO: 2 together with one or more biologically acceptable diluents, carriers or excipients therefor.

For purposes of the present invention, as disclosed and claimed herein, the following terms and abbreviations are defined as follows:

Base pair (bp) -- refers to DNA or RNA. The abbreviations A, C, G, and T correspond to the 5'-monophosphate forms of the nucleotides (deoxy)adenine, (deoxy)cytidine, (deoxy)guanine, and (deoxy)thymine, respectively, when they occur in DNA molecules. The abbreviations U, C, G, and T correspond to the 5'-monophosphate forms of the nucleosides uracil, cytidine, guanine, and thymine, respectively when they occur in RNA molecules. In double stranded DNA, base pair may refer to a partnership of A with T or C with G. In a DNA/RNA heteroduplex, base

pair may refer to a partnership of T with U or C with G.

DNA -- Deoxyribonucleic acid.

RNA -- Ribonucleic acid

Nucleic acid molecule -- DNA or RNA.

Plasmid -- an extrachromosomal self-replicating genetic element.

Reading frame -- the nucleotide sequence from which translation occurs "read" in triplets by the translational apparatus of tRNA, ribosomes and associated factors, each triplet corresponding to a particular amino acid. Because each triplet is distinct and of the same length, the coding sequence must be a multiple of three. A base pair insertion or deletion (termed a frameshift mutation) may result in two different proteins being coded for by the same DNA segment. To insure against this, the triplet codons corresponding to the desired polypeptide must be aligned in multiples of three from the initiation codon, i.e. the correct "reading frame" must be maintained. In the creation of fusion proteins containing a chelating peptide, the reading frame of the DNA sequence encoding the structural protein must be maintained in the DNA sequence encoding the chelating peptide.

Recombinant DNA Cloning Vector -- any autonomously replicating agent including, but not limited to, plasmids and phages, comprising a DNA molecule to which one or more additional DNA segments can or have been added.

Recombinant DNA Expression Vector -- any recombinant DNA cloning vector in which a promoter has been incorporated.

Recombinant Host Cell -- Any cell transformed using a recombinant DNA Vector and which is capable of either replicating or transcribing and translating DNA used to construct the recombinant DNA Vector.

Replicon -- A DNA sequence that controls and allows for autonomous replication of a plasmid or other vector.

Transcription -- the process whereby information contained in a nucleotide sequence of DNA is transferred to a complementary RNA sequence.

Translation -- the process whereby the genetic information of messenger RNA is used to specify and direct the synthesis of a polypeptide chain.

Treating -- describes the management and care of a human or veterinary patient for the purpose of combating a disease, condition, or disorder, of the patient. Treating includes the administration of a compound of present invention to prevent the onset of the symptoms or complications, alleviating the symptoms or complications, eliminating the disease, condition, or disorder. Treating therefor includes the inhibition of food intake, the inhibition of weight gain, and inducing weight loss in patients in need thereof.

Vector -- a replicon used for the transformation of cells in gene manipulation bearing polynucleotide sequences corresponding to appropriate protein molecules which, when combined with appropriate control sequences, confer specific properties on the host cell to be transformed. Plasmids, viruses, and bacteriophage are suitable vectors, since they are replicons in their own right. Artificial vectors are constructed by cutting and joining DNA molecules from different sources using restriction enzymes and ligases. Vectors include Recombinant DNA cloning vectors and Recombinant DNA expression vectors.

The amino acids abbreviations are accepted by the United States Patent and Trademark Office as set forth in 37 C.F.R. § 1.822 (b) (2) (1993). Unless otherwise indicated the amino acids are in the L configuration.

In one embodiment, the invention provides nucleic acid molecules that encode a novel *Rhesus ob* gene product which is defined by the following amino acid sequence.

SEQ ID NO: 2

1 5 10 15  
 Val Pro Ile Gln Lys Val Gln Ser Asp Thr Lys Thr Leu Ile Lys  
 20 25 30  
 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val  
 35 40 45  
 Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu  
 50 55 60  
 His Pro Val Leu Thr Leu Ser Gln Met Asp Gln Thr Leu Ala Ile  
 65 70 75  
 Tyr Gln Gln Ile Leu Ile Asn Leu Pro Ser Arg Asn Val Ile Gln  
 80 85 90  
 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu  
 95 100 105  
 25  
 Ala Phe Ser Lys Ser Cys His Leu Pro Leu Ala Ser Gly Leu Glu  
 110 115 120  
 Thr Leu Glu Ser Leu Gly Asp Val Leu Glu Ala Ser Leu Tyr Ser  
 30 125 130 135  
 Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp  
 140 145  
 Met Leu Trp Gln Leu Asp Leu Ser Pro Gly Cys-COOH  
 35

A preferred coding region for the above embodiment is defined by the following DNA sequence.

SEQ ID NO: 1

40  
 5' - GTG CCC ATC CAA AAA GTC CAA AGT GAC ACC AAA ACC CTC ATC  
 45 AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCG  
 GTC TCC TCC AAA CAG AGG GTC ACT GGT TTG GAC TTC ATT CCT GGG  
 CTC CAC CCC GTC CTG ACC TTA TCC CAG ATG GAC CAG ACA CTG GCA  
 ATC TAC CAA CAG ATC CTC ATC AAT CTG CCT TCC AGA AAC GTG ATC  
 50 CAA ATA TCC AAC GAC TTG GAG AAT CTC CGG GAC CTT CTT CAC CTG  
 CTG GCC TTC TCT AAG AGC TGC CAT TTG CCC TTG GCC AGT GGC CTG  
 GAG ACC TTG GAG AGC CTG GGG GAT GTC CTG GAA GCT TCA CTC TAC  
 55 TCC ACG GAG GTG GTG GCC CTG AGC AGG CTG CAG GGG TCT CTG CAG  
 GAC ATG CTG TGG CAG CTG GAC CTC AGC CCT GGG TGC - 3'

The proteins of the present invention may be produced either by recombinant DNA technology or well known chemical procedures, such as solution or solid-phase peptide synthesis, or semi-synthesis in solution beginning with protein fragments coupled through conventional solution methods.

The principles of solid phase chemical synthesis of polypeptides are well known in the art and may be found in general texts in the area such as Dugas, H. and Penney, C., Bioorganic Chemistry Springer-Verlag, New York, pgs. 54-92 (1981). For example, peptides may be synthesized by solid-phase methodology utilizing an PE-Applied Biosystems 430A peptide synthesizer (commercially available from Applied Biosystems, Foster City California) and synthesis cycles supplied by Applied Biosystems. Boc amino acids and other reagents are commercially available from PE-Applied Biosystems and other chemical supply houses. Sequential Boc chemistry using double couple protocols are applied to the starting p-methyl benzhydryl amine resins for the production of C-terminal carboxamides. For the production of C-terminal acids, the corresponding PAM resin is used. Arginine, Asparagine, Glutamine, Histidine and Methionine are coupled using performed hydroxy benzotriazole esters. The following side chain protection may be used:

Arg, Tosyl  
Asp, cyclohexyl or benzyl  
Cys, 4-methylbenzyl  
Glu, cyclohexyl  
His, benzyloxymethyl  
Lys, 2-chlorobenzyloxycarbonyl  
Met, sulfoxide  
Ser, Benzyl  
Thr, Benzyl  
Trp, formyl  
Tyr, 4-bromo carbobenzoxy

Boc deprotection may be accomplished with trifluoroacetic acid (TFA) in methylene chloride. Formyl removal from Trp is accomplished by treatment of the peptidyl resin with 20% piperidine in dimethylformamide for 60 minutes at 4°C. Met(O) can be reduced by treatment of the peptidyl resin with TFA/dimethylsulfide/conHCl (95/5/1) at 25°C for 60 minutes. Following the above pre-treatments, the peptides may be further deprotected and cleaved from the resin with anhydrous hydrogen fluoride containing a mixture of 10% m-cresol or m-cresol/10% p-thiocresol or m-cresol/p-thiocresol/ dimethylsulfide. Cleavage of the side chain protecting group(s) and of the peptide from the resin is carried out at zero degrees Centigrade or below, preferably -20°C for thirty minutes followed by thirty minutes at 0°C. After removal of the HF, the peptide/resin is washed with ether. The peptide is extracted with glacial acetic acid and lyophilized. Purification is accomplished by reverse-phase C18 chromatography (Vydac) column in .1% TFA with a gradient of increasing acetonitrile concentration. One skilled in the art recognizes that the solid phase synthesis could also be accomplished using the Fmoc strategy and a TFA/scavenger cleavage mixture.

The claimed DNA sequences are useful for expressing the *Rhesus ob* gene product either by direct expression or as fusion protein. When the claimed sequences are used in a fusion gene, the resulting product will require enzymatic or chemical cleavage. A variety of peptidases which cleave a polypeptide at specific sites or digest the peptides from the amino or carboxy termini (e.g. diaminopeptidase) of the peptide chain are known. Furthermore, particular chemicals (e.g. cyanogen bromide) will cleave a polypeptide chain at specific sites. The skilled artisan will appreciate the modifications necessary to the amino acid sequence (and synthetic or semi-synthetic coding sequence if recombinant means are employed) to incorporate site-specific internal cleavage sites. See U.S. Patent No. 5,126,249; Carter P., Site Specific Proteolysis of Fusion Proteins, Ch. 13 in Protein Purification: From Molecular Mechanisms to Large Scale Processes, American Chemical Soc., Washington, D.C. (1990).

Construction of suitable vectors containing the desired coding and control sequences employ standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated in the form desired to form the plasmids required.

To effect the translation of the desired protein, one inserts the engineered synthetic DNA sequence in any of a plethora of appropriate recombinant DNA expression vectors through the use of appropriate restriction endonucleases. The claimed protein is a relatively large protein. A synthetic coding sequence is designed to possess restriction endonuclease cleavage sites at either end of the transcript to facilitate isolation from and integration into these expression and amplification and expression plasmids. The isolated cDNA coding sequence may be readily modified by the use of synthetic linkers to facilitate the incorporation of this sequence into the desired cloning vectors by techniques well known in the art. The particular endonucleases employed will be dictated by the restriction endonuclease cleavage pattern of the parent expression vector to be employed. The restriction sites are chosen so as to properly orient the coding sequence with control sequences to achieve proper in-frame reading and expression of the claimed protein.

In general, plasmid vectors containing promoters and control sequences which are derived from species compatible with the host cell are used with these hosts. The vector ordinarily carries a replication origin as well as marker sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species (Bolivar, *et al.*, *Gene* 2: 95 (1977)). Plasmid pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR322 plasmid, or other microbial plasmid must also contain or be modified to contain promoters and other control elements commonly used in recombinant DNA technology.

The desired coding sequence is inserted into an expression vector in the proper orientation to be transcribed from a promoter and ribosome binding site, both of which should be functional in the host cell in which the protein is to be expressed. An example of such an expression vector is a plasmid described in Belagaje *et al.*, U.S. patent No. 5,304,493, the teachings of which are herein incorporated by reference. The gene encoding A-C-B proinsulin described in U.S. patent No. 5,304,493 can be removed from the plasmid pRB182 with restriction enzymes *Nde*I and *Bam*HI. The claimed DNA sequences of the present invention can be inserted into the plasmid backbone on a *Nde*I/*Bam*HI restriction fragment cassette.

In general, procaryotes are used for cloning of DNA sequences in constructing the vectors useful in the invention. For example, *E. coli* K12 strain 294 (ATCC No. 31446) is particularly useful. Other microbial strains which may be used include *E. coli* B and *E. coli* X1776 (ATCC No. 31537). These examples are illustrative rather than limiting.

Procaryotes also are used for expression. The aforementioned strains, as well as *E. coli* W3110 (prototrophic, ATCC No. 27325), bacilli such as *Bacillus subtilis*, and other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcescans*, and various pseudomonas species may be used. Promoters suitable for use with prokaryotic hosts include the b-lactamase (vector pGX2907 [ATCC 39344] contains the replicon and b-lactamase gene) and lactose promoter systems (Chang *et al.*, *Nature*, 275:615 (1978); and Goeddel *et al.*, *Nature* 281:544 (1979)), alkaline phosphatase, the tryptophan (*trp*) promoter system (vector pATH1 [ATCC 37695] is designed to facilitate expression of an open reading frame as a *trpE* fusion protein under control of the *trp* promoter) and hybrid promoters such as the *tac* promoter (isolatable from plasmid pDR540 ATCC-37282). However, other functional bacterial promoters, whose nucleotide sequences are generally known, enable one of skill in the art to ligate them to DNA encoding the protein using linkers or adaptors to supply any required restriction sites. Promoters for use in bacterial systems also will contain a Shine-Dalgarno sequence operably linked to the DNA encoding protein.

The claimed nucleic acid molecules may also be recombinantly produced in eukaryotic expression systems. Preferred promoters controlling transcription in mammalian host cells may be obtained from various sources, for example, the genomes of viruses such as: polyoma, Simian Virus 40 (SV40), adenovirus, retroviruses, hepatitis-B virus and most preferably cytomegalovirus, or from heterologous mammalian promoters, e.g. b-actin promoter. The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment which also contains the SV40 viral origin of replication. Fiers, *et al.*, *Nature*, 273:113 (1978). The entire SV40 genome may be obtained from plasmid pBRSV, ATCC 45019. The immediate early promoter of the human cytomegalovirus may be obtained from plasmid pCMBb (ATCC 77177). Of course, promoters from the host cell or related species also are useful herein.

Transcription of the claimed DNA by higher eucaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about 10-300 bp, that act on a promoter to increase its transcription. Enhancers are relatively oriented and positioned independently and have been found 5' (Laimins, L. *et al.*, *PNAS* 78:993 (1981)) and 3' (Lusky, M. L., *et al.*, *Mol. Cell Bio.* 3:1108 (1983)) to the transcription unit, within an intron (Banerji, J. L. *et al.*, *Cell* 33:729 (1983)) as well as within the coding sequence itself (Osborne, T. F., *et al.*, *Mol. Cell Bio.* 4:1293 (1984)). Many enhancer sequences are now known from mammalian genes (globin, RSV, SV40, EMC, elastase, albumin, a-fetoprotein and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 late enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription which may affect mRNA expression. These regions are transcribed as polyadenylated segments in the untranslated portion of the mRNA encoding protein. The 3' untranslated regions also include transcription termination sites.

Expression vectors may contain a selection gene, also termed a selectable marker. Examples of suitable selectable markers for mammalian cells are dihydrofolate reductase (DHFR, which may be derived from the *Bgl*II/*Hind*III restriction fragment of pJOD-10 [ATCC 68815]), thymidine kinase (herpes simplex virus thymidine kinase is contained on the *Bam*HI fragment of vP-5 clone [ATCC 2028]) or neomycin (G418) resistance genes (obtainable from pNNA14 yeast artificial chromosome vector [ATCC 37682]). When such selectable markers are successfully transferred into a mammalian host cell, the transfected mammalian host cell can survive if placed under selective pressure. There are two widely used distinct categories of selective regimes. The first category is based on a cell's metabolism and the use of a mutant cell line which lacks the ability to grow without a supplemented media. Two examples are: CHO DHFR<sup>-</sup> cells (ATCC CRL-9096) and mouse LTK<sup>-</sup> cells (L-M(TK<sup>-</sup>) ATCC CCL-2.3). These cells lack the ability to grow without the

addition of such nutrients as thymidine or hypoxanthine. Because these cells lack certain genes necessary for a complete nucleotide synthesis pathway, they cannot survive unless the missing nucleotides are provided in a supplemented media. An alternative to supplementing the media is to introduce an intact DHFR or TK gene into cells lacking the respective genes, thus altering their growth requirements. Individual cells which were not transformed with the DHFR or TK gene will not be capable of survival in nonsupplemented media.

The second category is dominant selection which refers to a selection scheme used in any cell type and does not require the use of a mutant cell line. These schemes typically use a drug to arrest growth of a host cell. Those cells which have a novel gene would express a protein conveying drug resistance and would survive the selection. Examples of such dominant selection use the drugs neomycin, Southern P. and Berg, P., J. Molec. Appl. Genet. 1: 327 (1982), mycophenolic acid, Mulligan, R. C. and Berg, P. Science 209:1422 (1980), or hygromycin, Sugden, B. et al., Mol Cell. Biol. 5:410-413 (1985). The three examples given above employ bacterial genes under eukaryotic control to convey resistance to the appropriate drug G418 or neomycin (geneticin), xgpt (mycophenolic acid) or hygromycin, respectively.

A preferred vector for eucaryotic expression is pRc/CMV. pRc/CMV is commercially available from Invitrogen Corporation, 3985 Sorrento Valley Blvd., San Diego, CA 92121. To confirm correct sequences in plasmids constructed, the ligation mixtures are used to transform E. coli K12 strain DH10B (ATCC 31446) and successful transformants selected by antibiotic resistance where appropriate. Plasmids from the transformants are prepared, analyzed by restriction and/or sequence by the method of Messing, et al., Nucleic Acids Res. 9:309 (1981).

Host cells may be transformed with the expression vectors of this invention and cultured in conventional nutrient media modified as is appropriate for inducing promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan. The techniques of transforming cells with the aforementioned vectors are well known in the art and may be found in such general references as Maniatis, et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (1989), or Current Protocols in Molecular Biology (1989) and supplements.

Preferred suitable host cells for expressing the vectors encoding the claimed proteins in higher eucaryotes include: African green monkey kidney line cell line transformed by SV40 (COS-7, ATCC CRL-1651); transformed human primary embryonal kidney cell line 293, (Graham, F. L. et al., J. Gen. Virol. 36:59-72 (1977), Virology 77:319-329, Virology 86:10-21); baby hamster kidney cells (BHK-21(C-13), ATCC CCL-10, Virology 16:147 (1962)); chinese hamster ovary cells CHO-DHFR<sup>-</sup> (ATCC CRL-9096), mouse Sertoli cells (TM4, ATCC CRL-1715, Biol. Reprod. 23:243-250 (1980)); african green monkey kidney cells (VERO 76, ATCC CRL-1587); human cervical epitheloid carcinoma cells (HeLa, ATCC CCL-2); canine kidney cells (MDCK, ATCC CCL-34); buffalo rat liver cells (BRL 3A, ATCC CRL-1442); human diploid lung cells (WI-38, ATCC CCL-75); human hepatocellular carcinoma cells (Hep G2, ATCC HB-8065); and mouse mammary tumor cells (MMT 060562, ATCC CCL51).

In addition to prokaryotes, unicellular eukaryotes such as yeast cultures may also be used. Saccharomyces cerevisiae, or common baker's yeast is the most commonly used eukaryotic microorganism, although a number of other strains are commonly available. For expression in Saccharomyces, the plasmid YRp7, for example, (ATCC-40053, Stinchcomb, et al., Nature 282:39 (1979); Kingsman et al., Gene 7:141 (1979); Tschemper et al., Gene 10:157 (1980)) is commonly used. This plasmid already contains the trp gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example ATCC no. 44076 or PEP4-1 (Jones, Genetics 85:12 (1977)).

Suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase (found on plasmid pAP12BD ATCC 53231 and described in U.S. Patent No. 4,935,350, June 19, 1990) or other glycolytic enzymes such as enolase (found on plasmid pAC1 ATCC 39532), glyceraldehyde-3-phosphate dehydrogenase (derived from plasmid pHcGAPC1 ATCC 57090, 57091), zymomonas mobilis (United States Patent No. 5,000,000 issued March 19, 1991), hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which contain inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein (contained on plasmid vector pCL28XhoLHBPV ATCC 39475, United States Patent No. 4,840,896), glyceraldehyde 3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose (GAL1 found on plasmid pRY121 ATCC 37658) utilization. Suitable vectors and promoters for use in yeast expression are further described in R. Hitzeman et al., European Patent Publication No. 73,657A. Yeast enhancers such as the UAS Gal from Saccharomyces cerevisiae (found in conjunction with the CYC1 promoter on plasmid YEpsec-hlIbeta ATCC 67024), also are advantageously used with yeast promoters.

The present invention provides a method for treating obesity. The method comprises administering to the organism an effective amount of anti-obesity protein in a dose between about 1 and 1000  $\mu\text{g/kg}$ . A preferred dose is from about

10 to 100  $\mu\text{g/kg}$  of active compound. A typical daily dose for an adult human is from about 0.5 to 100 mg. In practicing this method, the protein can be administered in a single daily dose or in multiple doses per day. The treatment regime may require administration over extended periods of time. The amount per administered dose or the total amount administered will be determined by the physician and depend on such factors as the nature and severity of the disease, the age and general health of the patient and the tolerance of the patient to the compound.

The instant invention further provides pharmaceutical formulations comprising the protein, preferably in the form of a pharmaceutically acceptable salt, which can be formulated for parenteral administration for the therapeutic or prophylactic treatment of obesity. For example, the protein can be admixed with conventional pharmaceutical carriers and excipients. The compositions comprising claimed proteins contain from about 0.1 to 90% by weight of the active protein, preferably in a soluble form, and more generally from about 10 to 30%. Furthermore, the present proteins may be administered alone or in combination with other anti-obesity agents or agents useful in treating diabetes.

For intravenous (IV) use, the protein is administered in commonly used intravenous fluid(s) and administered by infusion. Such fluids, for example, physiological saline, Ringer's solution or 5% dextrose solution can be used.

For intramuscular preparations, a sterile formulation, preferably a suitable soluble salt form of the protein, for example the hydrochloride salt, can be dissolved and administered in a pharmaceutical diluent such as pyrogenfree water (distilled), physiological saline or 5% glucose solution. A suitable insoluble form of the compound may be prepared and administered as a suspension in an aqueous base or a pharmaceutically acceptable oil base, e.g. an ester of a long chain fatty acid such as ethyl oleate.

The following examples will help describe how the invention is practiced and will illustrate the characteristics of the claimed DNA molecules, vectors, host cells, and methods of the invention.

### EXAMPLE 1

#### PCR Amplification

Degenerate primers were designed based on the published DNA sequence of region flanking the human *ob* gene. The primers were prepared for use in polymerase chain reaction (PCR) amplification methods using a Model 380A DNA synthesizers (PE-Applied Biosystems, Inc., 850 Lincoln Center Drive, Foster City, CA 94404). Forward primer: 5'-CCC AAG AAG CCC ATC CTG GGA AGG AAA ATG-3' (SEQ ID NO: 3) and reverse primer: 5'-CTT GCA GGA AGA GTG ACC TTC AAG GCC TCA-3' (SEQ ID NO: 4) were mixed together with PCR-ready *Rhesus* fat cell cDNA as the template prepared in the following manner.

*Rhesus* monkey adipose tissue was obtained from two individuals (designated 2810 and 2820) which are a part of a colony of *Rhesus* monkeys housed in Eli Lilly and Company's toxicology labs in Greenfield Indiana. Both samples of adipose tissue were handled identically and worked on in parallel. Total RNA was isolated using guanidine thiocyanate and ultracentrifugation method. The cDNA was synthesized using 5  $\mu\text{g}$  of total RNA and the SuperScript preamplification system commercially available from GIBCO-BRL (Grand Island, New York). Reverse transcription was primed with oligo dT primers provided in the kit.

PCR amplification was performed by mixing 2  $\mu\text{L}$  of cDNA generated in the reverse transcription step with approximately 20 pmoles of forward and reverse primers, and 2 units of Vent DNA polymerase® (New England Biolabs). The amplification was carried out in 35 amplification cycles (94°C-30 sec, 57°C-30 sec, 72°C-45 sec) preceded by HotStart at 80°C.

The PCR product was gel purified and cloned into a pCR-SCRIPT® cloning vector (Stratagene). The vector was then used to transform *E. coli* cells. Plasmid DNA was isolated from several white colonies and sequenced using standard DNA sequencing methods.

### Example 2

#### Vector Construction

A plasmid containing the DNA sequence encoding the desired claimed protein is constructed to include NdeI and BamHI restriction sites. The plasmid carrying the cloned PCR product is digested with MunI and BamHI restriction enzymes. The small ~ 400 bp fragment is gel-purified. The synthetic oligonucleotide linker is used to reconstruct the front part of the DNA up to MunI site and to introduce NdeI restriction sight and codons for Met-Arg. The synthetic linker, the 400 bp fragment, and pBR182 vector whose A-C-B proinsulin coding region is absent are ligated in a three piece ligation.

The ligation products are transformed into *E. coli* DH10B (commercially available from GIBCO-BRL) and colonies growing on tryptone-yeast (DIFCO) plates supplemented with 10 mg/mL of tetracycline are analyzed. Plasmid DNA is isolated, digested with NdeI and BamHI and the resulting fragments are separated by agarose gel electrophoresis.



Plasmids containing the expected ~ 400bp NdeI to BamHI fragment are kept. E. coli K12 RV308 (available from the NRRL under deposit number B-15624) are transformed with this second plasmid, resulting in a culture suitable for expressing the protein.

The techniques of transforming cells with the aforementioned vectors are well known in the art and may be found in such general references as Maniatis, et al. (1988) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York or Current Protocols in Molecular Biology (1989) and supplements. The techniques involved in the transformation of E. coli cells used in the preferred practice of the invention as exemplified herein are well known in the art. The precise conditions under which the transformed E. coli cells are cultured is dependent on the nature of the E. coli host cell line and the expression or cloning vectors employed. For example, vectors which incorporate thermoinducible promoter-operator regions, such as the c1857 thermoinducible lambda-phage promoter-operator region, require a temperature shift from about 30 to about 40 degrees C. in the culture conditions so as to induce protein synthesis.

In the preferred embodiment of the invention, E. coli K12 RV308 cells are employed as host cells but numerous other cell lines are available such as, but not limited to, E. coli K12 L201, L687, L693, L507, L640, L641, L695, L814 (E. coli B). The transformed host cells are then plated on appropriate media under the selective pressure of the antibiotic corresponding to the resistance gene present on the expression plasmid. The cultures are then incubated for a time and temperature appropriate to the host cell line employed.

Proteins which are expressed in high-level bacterial expression systems characteristically aggregate in granules or inclusion bodies which contain high levels of the overexpressed protein. Kreuger et al., in Protein Folding, Gierasch and King, eds., pgs 136-142 (1990), American Association for the Advancement of Science Publication No. 89-18S, Washington, D.C. Such protein aggregates must be solubilized to provide further purification and isolation of the desired protein product. Id. A variety of techniques using strongly denaturing solutions such as guanidinium-HCl and/or weakly denaturing solutions such as dithiothreitol (DTT) are used to solubilize the proteins. Gradual removal of the denaturing agents (often by dialysis) in a solution allows the denatured protein to assume its native conformation. The particular conditions for denaturation and folding are determined by the particular protein expression system and/or the protein in question.

Preferably, the present DNA sequences are expressed with a dipeptide leader sequence encoding Met-Arg or Met-Tyr as described in U.S. Patent No. 5,126,249, herein incorporated by reference. This approach facilitates the efficient expression of proteins and enables rapid conversion to the active protein form with Cathepsin C or other dipeptidylpeptidases. The purification of proteins is by techniques known in the art and includes reverse phase chromatography, affinity chromatography, and size exclusion.

### EXAMPLE 3

#### Biological Testing

Parabolic experiments suggest that a protein is released by peripheral adipose tissue and that the protein is able to control body weight gain in normal, as well as obese mice. Therefore, the most closely related biological test is to inject the test article by any of several routes of administration (i.v., s.c., i.m., i.p., or by minipump or cannula) and then to monitor food and water consumption, body weight gain, plasma chemistry or hormones (glucose, insulin, ACTH, corticosterone, GH, T4) over various time periods.

Suitable test animals include normal mice (ICR, etc.) and obese mice (*ob/ob*, *Avy/a*, *KK-Ay*, *tubby*, *fat*). The *ob/ob* mouse model of obesity and diabetes is generally accepted in the art as being indicative of the obesity condition. Controls for non-specific effects for these injections are done using vehicle with or without the active agent of similar composition in the same animal monitoring the same parameters or the active agent itself in animals that are thought to lack the receptor (*db/db* mice, *fa/fa* or *cp/cp* rats). Proteins demonstrating activity in these models will demonstrate similar activity in other mammals, particularly humans.

Since the target tissue is expected to be the hypothalamus where food intake and lipogenic state are regulated, a similar model is to inject the test article directly into the brain (e.g. i.c.v. injection via lateral or third ventricles, or directly into specific hypothalamic nuclei (e.g. arcuate, paraventricular, perifornical nuclei). The same parameters as above could be measured, or the release of neurotransmitters that are known to regulate feeding or metabolism could be monitored (e.g. NPY, galanin, norepinephrine, dopamine, b-endorphin release).

Similar studies are accomplished in vitro using isolated hypothalamic tissue in a perfusion or tissue bath system. In this situation, the release of neurotransmitters or electrophysiological changes is monitored.

Proteins expressed by the claimed DNA sequences are believed to be active in at least one of the above biological tests and are anti-obesity agents. As such, the claimed DNA sequences are useful for preparing protein compositions for treating obesity and disorders implicated by obesity. However, the claimed DNA sequences are also useful for preparing immunogens to raise antibodies for diagnostic use.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: ELI LILLY AND COMPANY  
 (B) STREET: Lilly Corporate Center  
 (C) CITY: Indianapolis  
 (D) STATE: Indiana  
 (E) COUNTRY: United States of America  
 (F) ZIP: 46285

(ii) TITLE OF INVENTION: RHESUS OB PROTEIN AND DNA

(iii) NUMBER OF SEQUENCES: 4

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 (A) ADDRESSEE: C. M. Hudson  
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 (E) COUNTRY: United Kingdom  
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(v) COMPUTER READABLE FORM:  
 (A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: Macintosh  
 (C) OPERATING SYSTEM: Macintosh 7.0  
 (D) SOFTWARE: Microsoft Word 5.1

(vi) CURRENT APPLICATION DATA:  
 (A) APPLICATION NUMBER: 96303601.7

## (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 438 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTG CCC ATC CAA AAA GTC CAA AGT GAC ACC AAA ACC CTC ATC AAG ACA  
 Val Pro Ile Gln Lys Val Gln Ser Asp Thr Lys Thr Leu Ile Lys Thr  
 1 5 10 15

ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCG GTC TCC TCC  
 Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser  
 20 25 30

5 AAA CAG AGG GTC ACT GGT TTG GAC TTC ATT CCT GGG CTC CAC CCC GTC 144  
 Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Val  
 35 40 45  
 CTG ACC TTA TCC CAG ATG GAC CAG ACA CTG GCA ATC TAC CAA CAG ATC 192  
 Leu Thr Leu Ser Gln Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile  
 50 55 60  
 10 CTC ATC AAT CTG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC GAC TTG 240  
 Leu Ile Asn Leu Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu  
 65 70 75 80  
 GAG AAT CTC CGG GAC CTT CTT CAC CTG CTG GCC TTC TCT AAG AGC TGC 288  
 Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys  
 85 90 95  
 15 CAT TTG CCC TTG GCC AGT GGC CTG GAG ACC TTG GAG AGC CTG GGG GAT 336  
 His Leu Pro Leu Ala Ser Gly Leu Glu Thr Leu Glu Ser Leu Gly Asp  
 100 105 110  
 20 GTC CTG GAA GCT TCA CTC TAC TCC ACG GAG GTG GTG GCC CTG AGC AGG 384  
 Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg  
 115 120 125  
 CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC CTC AGC CCT 432  
 Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro  
 130 135 140  
 GGG TGC 438  
 Gly Cys  
 145  
 30

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

40 Val Pro Ile Gln Lys Val Gln Ser Asp Thr Lys Thr Leu Ile Lys Thr  
 1 5 10 15  
 Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser  
 20 25 30  
 45 Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Val  
 35 40 45  
 Leu Thr Leu Ser Gln Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile  
 50 55 60  
 Leu Ile Asn Leu Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu  
 65 70 75 80  
 Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys  
 85 90 95  
 55

His Leu Pro Leu Ala Ser Gly Leu Glu Thr Leu Glu Ser Leu Gly Asp  
100 105 110

5 Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg  
115 120 125

Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro  
130 135 140

10 Gly Cys  
145

(2) INFORMATION FOR SEQ ID NO: 3:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

25 CCCAAGAAGC CCATCCTGGG AAGGAAAATG

30

(2) INFORMATION FOR SEQ ID NO: 4:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

40 CTTGCAGGAA GAGTGACCTT CAAGGCCTCA

30

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## Claims

1. A protein of the formula:

5  
 10  
 15  
 NH<sub>2</sub>-Val Pro Ile Gln Lys Val Gln Ser Asp Thr Lys Thr Leu Ile  
 Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser  
 Val Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly  
 Leu His Pro Val Leu Thr Leu Ser Gln Met Asp Gln Thr Leu Ala  
 Ile Tyr Gln Gln Ile Leu Ile Asn Leu Pro Ser Arg Asn Val Ile  
 Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu  
 Leu Ala Phe Ser Lys Ser Cys His Leu Pro Leu Ala Ser Gly Leu  
 Glu Thr Leu Glu Ser Leu Gly Asp Val Leu Glu Ala Ser Leu Tyr  
 Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln  
 Asp Met Leu Trp Gln Leu Asp Leu Ser Pro Gly Cys-COOH  
 (SEQ ID NO: 2).

or a pharmaceutically acceptable salt thereof.

- 20  
 25  
 30  
 35  
 40  
 2. A method of treating obesity, which comprises administering to a mammal in need thereof a protein of Claim 1.  
 3. A pharmaceutical formulation, which comprises a protein of Claim 1 together with one or more pharmaceutical acceptable diluents, carriers or excipients therefor.  
 4. An isolated nucleic acid molecule consisting of a nucleotide sequence that encodes the protein of Claim 1.  
 5. A nucleic acid molecule of Claim 4 consisting of DNA having the following nucleotide sequence:

30  
 35  
 40  
 5' - GTG CCC ATC CAA AAA GTC CAA AGT GAC ACC AAA ACC CTC ATC  
 AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCG  
 GTC TCC TCC AAA CAG AGG GTC ACT GGT TTG GAC TTC ATT CCT GGG  
 CTC CAC CCC GTC CTG ACC TTA TCC CAG ATG GAC CAG ACA CTG GCA  
 ATC TAC CAA CAG ATC CTC ATC AAT CTG CCT TCC AGA AAC GTG ATC  
 CAA ATA TCC AAC GAC TTG GAG AAT CTC CGG GAC CTT CTT CAC CTG  
 CTG GCC TTC TCT AAG AGC TGC CAT TTG CCC TTG GCC AGT GGC CTG  
 GAG ACC TTG GAG AGC CTG GGG GAT GTC CTG GAA GCT TCA CTC TAC  
 TCC ACG GAG GTG GTG GCC CTG AGC AGG CTG CAG GGG TCT CTG CAG  
 GAC ATG CTG TGG CAG CTG GAC CTC AGC CCT GGG TGC - 3'  
 (SEQ ID NO: 1)

- 45  
 50  
 55  
 6. A recombinant DNA vector comprising a nucleic acid molecule of Claim 4.  
 7. A recombinant DNA vector comprising the DNA molecule of Claim 5.  
 8. A recombinant host cell comprising a vector of Claim 6.  
 9. A recombinant host cell comprising a vector of Claim 7.  
 10. A process for producing an anti-obesity protein comprising;  
 a) culturing a host cell of any one of Claims 8 or 9 under suitable protein expression conditions; and,  
 b) isolating a protein comprising an amino acid sequence of SEQ ID NO: 2.

(19)



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(11)

**EP 0 744 408 A3**

(12)

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(51) Int Cl.<sup>6</sup>: **C12N 15/12, C12N 15/70,  
C12N 1/21, C07K 14/00,  
A61K 38/17  
// (C12N1/21, C12R1:19)**

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(54) **Rhesus ob protein and DNA**

(57) The invention includes proteins, pharmaceutical formulations, and methods useful for expressing pro-

teins that regulate the body's volume of adipose tissue. In particular, the *Rhesus ob* gene and gene product are disclosed.

**EP 0 744 408 A3**



European Patent  
Office

# PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention EP 96 30 3601  
shall be considered, for the purposes of subsequent  
proceedings, as the European search report

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
X	NATURE, vol. 372, no. 6505, 1 December 1994, LONDON GB, pages 425-432, XP002003607 Y. ZHANG ET AL.: "Positional cloning of the mouse obese gene and its human homolog" * page 431, left-hand column, paragraph 2 - right-hand column, last paragraph; figures 4,6 *	1	C12N15/12 C12N15/70 C12N1/21 C07K14/00 A61K38/17 /(C12N1/21, C12R1:19)
X	BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 209, no. 3, 26 April 1995, DULUTH, MINNESOTA US, pages 944-952, XP002014741 T. MURAKAMI AND K. SHIMA: "Cloning of the rat obese cDNA and its expression in obese rats" * figure 2 *	1	<p>TECHNICAL FIELDS SEARCHED (Int.Cl.6)</p> <p>C07K A61K</p>
<p>INCOMPLETE SEARCH</p> <p>The Search Division considers that the present European patent application does not comply with the provisions of the European Patent Convention to such an extent that it is not possible to carry out a meaningful search into the state of the art on the basis of some of the claims</p> <p>Claims searched completely :</p> <p>Claims searched incompletely :</p> <p>Claims not searched :</p> <p>Reason for the limitation of the search:</p> <p>see sheet C</p>			
Place of search		Date of completion of the search	Examiner
THE HAGUE		30 September 1996	Fuhr, C
CATEGORY OF CITED DOCUMENTS		<p>T : theory or principle underlying the invention</p> <p>E : earlier patent document, but published on, or after the filing date</p> <p>D : document cited in the application</p> <p>L : document cited for other reasons</p> <p>&amp; : member of the same patent family, corresponding document</p>	
<p>X : particularly relevant if taken alone</p> <p>Y : particularly relevant if combined with another document of the same category</p> <p>A : technological background</p> <p>O : non-written disclosure</p> <p>P : intermediate document</p>			

EPO FORM 150 (03.92) (P4C07)



European Patent  
Office

## PARTIAL EUROPEAN SEARCH REPORT

Application Number

EP 96 30 3601

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
P,X	WO-A-96 05309 (UNIV ROCKEFELLER ; FRIEDMAN JEFFREY M (US); ZHANG YIYING (US); PROE) 22 February 1996 * claims; examples *	1-10	
E	EP-A-0 725 078 (LILLY CO ELI) 7 August 1996 * claims; examples *	1-10	
A	EP-A-0 566 410 (SANKYO CO) 20 October 1993 * page 2, line 1 - line 9; claims; examples *	1-10	
			TECHNICAL FIELDS SEARCHED (Int.Cl.6)

EPO FORM 1503 01.82 (P04 C10)





EP 96 30 3601

-C-

Remark: Although claim 2  
is directed to a method of  
treatment of the human/animal  
body (Art. 52(4) EPC) the search  
has been carried out and based on  
the alleged effects of the  
compound/composition